

M	L	A	G	G	V	R															
GAG	CCC	GGG	TCT	TTT	CCT	CCC	AGC	ATG	CTG	CCC	CCC	CCC	CTG	AGG	151						
S	M	P	S	P	L	L	A	C	W	Q	P	I	L	L	V	L	G	S	27		
AGC	ATG	CCC	AGC	CCC	CTG	CTG	CCC	CCC	TCC	TCC	TGG	CAG	CCC	ATG	CTG	CTG	CTG	GGC	TCA	211	
V	L	S	G	S	A	T	G	C	P	P	R	C	E	C	S	A	Q	D	R	47	
GTG	CTG	TCA	GGC	TCC	GGC	ACG	GGC	TCC	CCC	CCC	CCC	TCC	CAG	TGC	TCC	CCC	CCC	CAG	GAC	CCC	271
A	V	L	C	H	R	K	R	F	V	A	V	P	E	G	I	P	T	E	T	67	
GCT	CTG	CTG	TGC	CAC	CCC	AAG	CCC	TTT	GTC	GGC	GCA	GTC	CCC	CAG	GGC	ATC	CCC	ACC	GAG	ACG	331
R	L	L	D	L	G	K	N	R	I	K	T	L	N	Q	D	E	F	A	S	37	
CCC	CTG	GAC	CTA	GGC	AAG	AAC	CCC	ATC	AAA	ACG	CTC	AAC	CAG	GAC	CAG	TTC	GGC	AGC	391		
F	P	H	L	E	S	L	E	L	N	E	N	I	V	S	A	V	E	P	G	107	
TTC	CCC	CAC	CTG	GAG	GAG	CTG	GAG	CTC	AAC	CAG	AAC	ATC	GTC	AGC	CCC	CTG	GAG	CCC	CCC	451	
A	F	N	N	L	F	N	L	R	T	L	G	L	R	S	N	R	L	K	L	127	
CCC	TTC	AAC	AAC	CTC	TTC	AAC	CTC	CGG	ACG	CTG	GGT	CTC	CCC	AGC	AAC	CCC	CTG	AAG	CTC	511	
I	P	L	G	V	F	T	G	L	S	N	L	T	K	L	D	T	R	E	N	147	
ATC	CCC	CTA	GGC	GTC	TTC	ACT	GGC	CTC	AGC	AAC	CTG	ACC	AAG	CTG	GAC	ACG	AGG	GAG	AAC	571	
K	I	V	I	L	L	D	Y	M	F	Q	D	L	Y	N	L	K	S	L	E	167	
AAG	ATC	GTC	ATC	CTA	CTG	GAC	TAC	ATG	TTT	CAG	GAC	CTG	TAC	AAC	CTC	AAG	TCA	CTG	GAG	531	
V	G	D	N	D	L	V	Y	I	S	H	R	A	F	S	G	L	N	S	L	187	
GTG	GGC	GAC	AAT	GAC	CTC	GTC	TAC	ATC	TCT	CAC	CCC	CCC	TTC	AGC	GGC	CTC	AAC	AGC	CTG	591	
E	Q	L	T	L	E	K	C	N	L	T	S	I	P	T	E	A	L	S	H	207	
CAG	CAG	CTG	ACT	CTG	GAG	AAA	TGC	AAC	CTG	ACC	TCC	ATC	CCC	ACC	GAG	GGG	CTG	TCC	CAC	751	
L	H	G	L	I	V	L	R	L	R	H	L	N	I	N	A	I	R	D	Y	227	
CTG	CAC	GGC	CTC	ATC	GTC	CTG	AGG	CTC	CGG	CAC	CTC	AAC	ATC	AAT	GCC	ATC	CGG	GAC	TAC	311	
S	F	K	R	L	Y	R	L	K	V	L	E	I	S	H	W	P	Y	L	D	247	
TTC	TTC	AAG	AGG	CTG	TAC	CGA	CTC	AAG	GTC	TTG	GAG	ATC	TCC	CAC	TGG	CCC	TAC	TTG	GAC	371	
T	M	T	P	N	C	L	Y	G	L	N	L	T	S	L	S	I	T	H	C	267	
ACC	ATG	ACA	CCC	AAC	TCC	CTC	TAC	GGC	CTC	AAC	CTG	AGC	TCC	CTG	TCC	ATC	ACA	CAC	TCC	931	
N	L	T	A	V	P	Y	L	A	V	R	H	L	V	Y	L	R	F	L	N	287	
AAT	CTG	ACC	GCT	GTC	CCC	TAC	CTG	GCC	GTC	CCC	CAC	CTA	GTC	TAT	CTC	GGC	TTC	CTC	AAC	991	
L	S	Y	N	P	I	S	T	I	E	G	S	M	L	H	E	L	L	R	L	307	
CTC	TCC	TAC	AAC	CCC	ATC	AGC	ACC	ATT	GAG	GGC	TCC	ATG	TTG	CAT	GAG	CTG	CTC	CGG	CTG	1051	
Q	E	I	Q	L	V	G	G	Q	L	A	V	V	E	P	Y	A	F	R	G	327	
CAG	GAG	ATC	CAG	CTG	GTC	GGC	CGG	CAG	CTG	GGC	CTG	GAG	CCC	TAT	GCC	TTC	GGC	GGC	1111		
L	N	Y	L	R	V	L	N	V	S	G	N	Q	L	T	T	L	E	E	S	347	
CTC	AAC	TAC	CTG	GGC	GTC	CTC	AAT	GTC	TCT	GGC	AAC	CAG	CTG	ACC	ACA	CTG	GAG	GAA	TCA	1171	

FIG. 1A

FIG. 1B

FIG. 2

Percent Similarity: 49.308 Percent Identity: 29.412

T79 1 MLAGGVRSMPSPLLACWQPILLVLGSVLSGS..ATGCPPRCECSAQDR. 47
D45913 1MARLSTGKAAC.QVVLGLLITSLTESSILTSECQLCVCEIRPWF 44

T79 48AVLCHRKRKVAVPEGIPTETRLLDLGKNRIKTLNQDEFAS 87
D45913 45 TPQSTYREATTVDNDLRLTRIPGNLSSDTQVLLQSNNI..... 84

T79 88 FPHLEELNENIVSAVEPGAFNNLFNLRTLGLRSNRLKLIPLGVFTGLS 137
D45913 85AKTVDDELQQLFNLTELDLFSQNNFTNIKEVGLANLT 119

T79 138 NLTKLDTRENKIVILLYMFQDLYNLKSLEVGDNDLVYISHRAFSGLNSL 187
D45913 120 QLTTLHLEENQISEMTDYCLQDLSNLQELYINHNQISTISANAFSGLKNL 169

T79 188 EQLTLEKCNLTSIPTEAALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKV 237
D45913 170 LRLHLNSNKLKVIDSRWFDSTPNLEILMIGENPVIGILDMMFRPLSNLRS 219

T79 238 LEISHWPYLDTMTPNCLYGLN.LTLSITHCNLTAVPYLAVRHLVYLRF 286
D45913 220 LVLAG.MYLTDPGNALVGLDSLESLSFYDNKLIKVPQLALQKVPNLKFL 268

T79 287 NLSYNPISTIEGSMHLELLRLQEIQLVG.GQLAVVEPY..... 323
D45913 269 DLNKNPIHKIQEGDFKNMLRLKELGINNMGELVSVDRYALDNLPETKLE 318

T79 324AFRGLNYLRVLNVSGNQLTLEESVFHSVGNELETLIL 360
D45913 319 ATNNPKLSYIHRLAFRSVPALESMLNNNALNAVYQKTVESLPNLREISI 368

T79 361 DSNPLACDCRLLWVFRWRNLNFNRQQPT.CATPEFVQGKEFKDFPDVLL 409
D45913 369 HSNPLRCDCVIHWINSNKTNIRFMEPLSMFCAMPPEYRGQQVK...EVLI 415

T79 410 PNYFT.CRRARIRDRKAQQVFVDEGHTVQFVCRADGDPPPAILWLSPRKH 458
D45913 416 QDSSEQCLPMISHDTFPNHLNMDIGTTFLDCRAMAEPEPEIYWVTPIGN 465

T79 459 LVSAKS.NGRLTVPDGTLEVRYAQVQDNGTYLCIAANAGGNDNSMPAHLH 507
D45913 466 KITVETLSDKYKLSSEGTLIANIQIEDSGRYTCVAQNVQGADTRVATIK 515

T79 508 V.....RSYSPDWPHQ 518
D45913 516 VNGTLLDGAQVLKIYVKQTESHSILVSWKVNSNVMTSNLKWWSSATMKIDN 565

T79 519 PNKTF.....AFISNQPGEGEANSTRA 540

FIG. 3A

D45913 566 |: |: . | .|...: .| |
PHITYTARVPVDVHEYNLTHLQPSTDYEVCLTVSNIHQQTQKSCVNVTX 615

T79 541 TYPFPFDIKTLIIATTMGI|.SFLGVVLFCVLFLWSRGKGNTHNIE 588
.:.|::||.. . .|.: : |:::|: : . : ::: .| | .. |:
D45913 616 TAAFALDISDHETSTALAAVMGSMFAVISLASIAIYIAKRFKRKNYHSL 665

T79 589 IEYVPRKSDAGISSADAPRKFNMKMI..... 614
.|:...|. |. :|:
D45913 666 KKYMQKTSSIPLNEL.YPPLINLWEADSDKDKDGSADTKPTQVDTSRSY 714

FIG. 3B

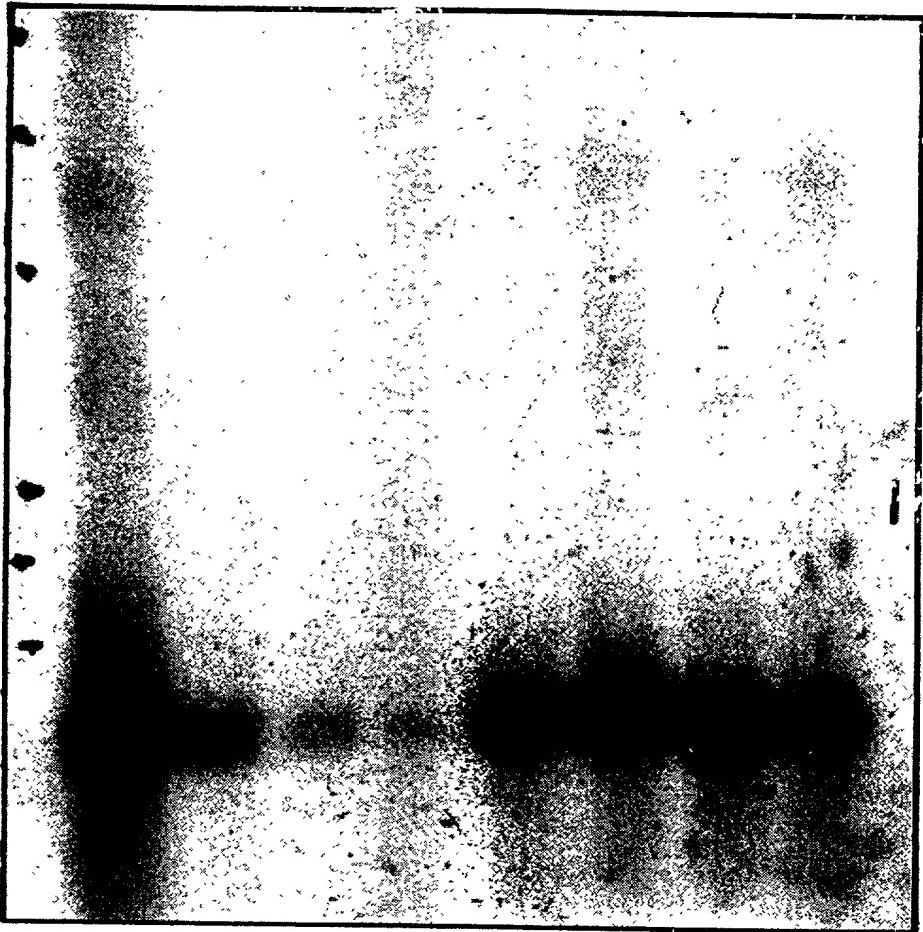


FIG. 4

T R P I L V I H D E Q K G P E V T S N	19
CC ACG CGT CCC ATC TTG GTC ATC CAC GAT GAA CAG AAG CGG CCC GAA GTG ACC TCC AAT	59
A A L T L R N F C N W Q K Q H N P P S D	39
GCT CCC CTC ACT CTC CGG AAC TTT TCC AAC TGG CAG AAG CAG CAC AAC CCA CCC AGT GAC	119
R D A E H Y D T A I L F T R Q D L C G S	59
CGG GAT GCA GAG CAC TAT GAC ACR GCA ATT CTT TTC ACC AGA CAG GAC TTG TGT CGG TCC	179
Q T C D T L G M A D V G T V C D P S R S	79
CAG ACA TGT GAT ACT CTT CGG ATG GCT GAT GTT CGA ACT GTG TGT GAT CGG AGC AGA ACC	239
C S V I E D D G L Q A A F T T A H E L G	99
TGC TCC GTC ATA GAA GAT GAT GGT TTA CAA GCT CCC TTC ACC ACR GCC CAT GAA TTA CGC	299
H V F N M P H D D A K Q C A S L N G V N	119
CAC GTG TTT AAC ATG CCA CAT GAT GCA AAG CAG TGT CGC AGC CTT AAT GGT GTG AAC	359
Q D S H M M A S M L S N L D H S Q P W S	139
CAG GAT TCC CAC ATG ATG CGG TCA ATG CTT TCC AAC CTC GAC CAC AGC CAG CCT TCG TCT	419
P C S A Y M I T S F L D N G H G E C L M	159
CCT TCC AGT GCC TAC ATG ATT ACA TCA TTT CTC GAT AAT GGT CAT CGG GAA TGT TTG ATG	479
D K P Q N P I Q L P G D L P G T S Y D A	179
GAC AAG CCT CGG AAT CGG ATA CGG CTC CCA CGC GAT CTC CCT CGC ACC TCG TAC GAT GCC	539
N R Q C Q F T F G E D S K H C P D A A S	199
AAC CGG CGG TCC CGG TTT ACA TTT CGG CGG GAC TCC AAA CAC TGC CCT GAT GCA GCC AGC	599
T C S T L W C T G T S G G V L V C Q T K	219
ACA TGT AGC ACC TTG TGG TGT ACC CGC ACC TCT TGT CGG CGG CGC TGT CGT TGT CAA ACC AAA	659
H F P W A D G T S C G E G K W C I N G K	239
CAC TTC CGG TGG CGG GAT CGC ACC AGC TGT CGA GAA CGG AAA TGG TGT ATC AAC CGC AAG	719
C V N K T D R K H F D T P F H G S W G M	259
TGT GTG AAC AAA ACC GAC AGA AAG CAT TTT GAT AGC CCT TTT CAT CGA AGC TGG CGA ATG	779
W G P W G D C S R T C G G G V Q Y T M R	279
TGG CGG CCT TGG CGA GAC TGT TCG AGA AGC TGC CGT CGG CGA GTC CGC CAG TAC ACG ATG AGG	839
E C D N P V P K N G G K Y C E G K R V R	299
GAA TGT GAC AAC CGA GTC CCA AAG AAT CGA CGG AAG TAC TGT GAA CGC AAA CGA GTG CGC	899
Y R S C N L E D C P D N N G K T F R E E	319
TAC AGA TCC TGT AAC CTT GAG GAC TGT CCA GAC AAT GGA AAA ACC TTT AGA GAG GAA	959
Q C E A H N E F S K A S F G S G P A V E	339
CAA TGT GAA CGA CGC AAC GAG TTT TCA AAA GCT TCC TTT CGG AGT CGG CCT CGG GTG GAA	1019
W I P K Y A G V S P K D R C K L I C Q A	359
TGG ATT CGC AAG TAC GCT CGC GTC TCA AAG GAC AGG TGC AAG CTC ATC TGC CAA CGC	1079
K G I G Y F F V L Q P K V V D G T P C S	379
AAA CGC ATT CGC TAC TTC TTG CAG CCC AAG GTT GIA GAT CGT ACT CGA TGT AGC	1139

FIG. 5A

P D S T S V C V Q G Q C V K A G C D R I 399
 CCA GAT TCC ACC TCT GTC TGT GTG CAA CGA CGG TGT GTA AAA CCT CGT TGT GAT CCC ATC 1199
 I D S K K K F D K C G V C G G N G S T C 419
 ATA GAC TCC AAA AAG AAC TTT GAT AAA TGT GGT GTT TCC CGG CGA AAT CGA TGT ACT TGT 1259
 K K I S G S V T S A K P G Y H D I I T I 439
 AAA AAA ATA TCA CGA TCA GTT ACT AGT CGA AAA CCT CGA TAT CAT GAT ATC ATC ACA ATT 1319
 P T G A T N I E V K Q R N Q R G S R N N 459
 CCA ACT CGA GCC ACC AAC ATC GAA GTG AAA CGG CGG AAC CGG AGG CGA TCC AGG AAC AAT 1379
 G S F L A I K A A D G T Y I L N G D Y T 479
 CGC AGC TTT CCTT GCC ATC AAA GCT GCT GAT CGC ACA TAT ATT CCTT AAT GGT GAC TAC ACT 1439
 L S T L E Q D I M Y K G V V L R Y S G S 499
 TTG TCC ACC TTA GAG CGA GAC ATT ATG TAC AAA CGT CCT GTC TTG AGG TAC AGC CGC TCC 1499
 S A A L E R I R S F S P L K E P L T I Q 519
 TCT CGG CGA TTG GAA AGA ATT CGC AGC TTT AGC CCT CTC AAA GAG CGC TTG ACC ATC CGG 1559
 V L T V G N A L R P K I K Y T Y F V K K 539
 GTT CCTT ACT GTG CGC AAT CGC CCTT CGA CCT AAA ATT AAA TAC ACC TAC TCC GCA AAG AAG 1619
 K K E S F N A I P T F S A W V I E E W G 559
 AAG AAG GAA TCT TTC AAT GCT ATC CGC ACT TTT TCA GCA TGG GTC ATT GAA GAG TGG CGC 1679
 E C S K T C G K G Y K K R S L K C L S H 579
 GAA TGT TCT AAG ACC TGT CGG AAG GGT TAC AAA AAA AGA AGC TTG AAG TGT CTG TCC CAT 1739
 D G G V L S H E S C D P L K K P K H F I 599
 GAT CGA CGG GTG TTA TCT CAT GAG AGC TGT GAT CCT TTA AAG AAA CCT AAA CAT TTC ATA 1799
 D F C T M A E C S * 609
 GAC TTT TGC ACA ATG GCA GAA TGC AGT TAA 1829
 GTGGTTAAGTGGTGTAGCTCTGAGGCCAGGCAAGTGAGGAAGGGCTGGCAGGGAAAGCAGGAGGCTGGAGGG 1908
 ATCCAGCGTATCTTCCCAGTAACCACTGAGGTGTATCAGTAAGGTGGATTATGGGGTAGATAAGAAAAGGAGTTGAAT 1987
 CTCAGAGTAACGCCAGTTGCAATTTCAGGGATAGTTAGTGAGGATTATTAACCTCTGAGCAGTGATATAGCATTA 2066
 ATTAAGCCCCGGCAATTATTATTATTCTTCTTGTACATCTTTACAAGTTTACAAAAACAAAGCAATTGTCAA 2145
 AAGAGTTGAACTTACAAACCCCCTTTCTGGTACTTTCAAAATCTTACTTGTATCTCTGGGGTTGGAAATGAAAAGT 2224
 AGGRGAAAGTGAGTTTACTAACGACTGTTTACTTTACCTCTCAACAAATGGGGGGAGAAGGAGTACAAATAGGA 2303
 TCCTTGACGCCAGCTGTTTACGCCCTATGGTTTCAAGAGAAATGTTTACATTATTTCTACCGAGAAATTAACTTCA 2382
 GATTCCTTACATGAGGAAAGGCTCGCAACGTGAAATAACGCAAAATGGCTTCTTCTTCTTCTTCTGACCTCTCA 2461
 GTCCTTATTTGTGTAATTCTTCTTCTGAGGAAAAACAACTCCATGTATTTCAGTGCAATTAAAGTCTCACATTGGAAA 2540
 AAAAGCAGTGAGGCAATTAGTGCTGGTAAAAGCTAGAGGGAGACACAATGAGCTTACGTCCTTACCTCCAACTTCCTTCTTCC 2619
 TACCGTGTACCCCTGTTGGAAATGGATGTAAGAAGTAACCTGTCCTCTGAAAATCACTACAAATCAGCACAGG 2698

FIG. 5B

ACCCATGAAACCCCGAAACAAAATCTGGTTTTCAGACGCGTTCGCGGATTCAGAATCTTTC	2777
TGGTGGGGGGGTGGCTGCGGGTGCGCTCTTCGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	2856
AGCTCTTTTGAGAAATGATTCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	2935
ATTCGGTTGGGTC	3014
ATTTCTATGAAAAAAACTTTTAAATTATCTGGCTTTTGGAAGTCGCTATAAAATAGACTTTTACATATGT	3093
TACTAGAAATAAAAGAACCTTTTGGAAAAAAGGGGGGGGG	3147

FIG. 5C

D
9
8
0
6
5
6
2
*
G
4
4
6
6
6
3

251 DQSMADFHDGSGLKHVLLTFSVAARFYKRPSTIRNSISLWWVKILVITYEQ 300
||||.::|||
1TRPILVIRDEQ 11

301 KGPEVTSAALTLRNFCSWQKQHNSPSDROPEHYDTAILFTRQDLGGSHT 350
|||||..|||||.|||||:|||||:|||||:
12 KGPEVTSAALTLRNFCNWQKQHNPSPSDRDAEYDTAILFTRQDLGGSQT 61

351 CDTLGADVGTVCDPSRSCSVIEDDGLQAAFTTAELGHVFNMPHDDAKH 400
|||||..|||||.|||||:|||||:
62 CDTLGADVGTVCDPSRSCSVIEDDGLQAAFTTAELGHVFNMPHDDAKQ 111

401 CASLNGVSGDSHIMASMLSSLDHSQPWSPCSAVMITSPLANGHGECLMDK 450
|||||..|||||.|||||:|||||:
112 CASLNGVNQDSHIMASMLSNLDHSQPWSPCSAVMITSPLANGHGECLMDK 161

451 PQNPIKLPSDLPGTYDANRQCQFTTGEESKHCPCDNASTCSTLNCTGTSG 500
|||||..|||||.|||||:|||||:
162 PQNPIKLPGDLPGTSYDANRQCQFTTGEESKHCPCDNASTCSTLNCTGTSG 211

501 GLLVCQTTKHFYWADGTSCEGGEGKWCVSGKCVNKTKMRIFATPVHGSGNGPNG 550
|:|||||..|||||.|||||:
212 GVLVCQTTKHFYWADGTSCEGGEGKWCINGKCVNKTKRIFATPVHGSGNG 261

551 PWGDCSRICGGVQYTMRRECINPVPRNGKRYCEGKRVRYRSCNIEDCPDN 600
|||||..|||||.|||||:
262 PWGDCSRICGGVQYTMRRECINPVPRNGKRYCEGKRVRYRSCNIEDCPDN 311

601 NGKTFREEQCEAHNEFSKASFGNEPTVENTPKYAGVSPKDRCKLTCEARG 650
|||||..|||||.|||||:
312 NGKTFREEQCEAHNEFSKASFGSGPAVENIPKYAGVSPKDRCKLICQAXG 361

651 IGYFFVLQPKVVDGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKFDKQGV 700
|||||..|||||.|||||:
362 IGYFFVLQPKVVDGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKFDKQGV 411

701 CGGNGSTCKKMSGIVTSTRPGYHDIVTIPAGAINIEVKHRNQRGSRNGS 750
|||||..|||||.|||||:
412 CGGNGSTCKKLSGSVTSAKPGYHDITIPTGAINIEVKQRNQRGSRNGS 461

751 FLAIKAADGTYILNGNFTLSTLEQDLTVXGTVLRYSGSSAALERIRSFSP 800
|||||..|||||.|||||:
462 FLAIKAADGTYILNGMTLSTLEQDLYKGVVLRYSGSSAALERIRSFSP 511

801 LKEPLTIQVLMUGHALRPICLQFTYFMKRTTESFNAIPTFSENVIEENGEC 850
|||||..|||||.|||||:
512 LKEPLTIQVLTGVNALRPICLQFTYFVKXXXXESFNAIPTFSAWVIEENGEC 560

901 WSPCSKTCGKGYKKRTLKCVSHDGGVLSNESCDPLKKPKHYIDFCILTQC 950
|||||..|||||.|||||:
561 ...CSKTCGKGYKKRSLKCLSHDGGVLSHESCDPLKKPKHFIDFCIMABC 607

951 S* 951
|
608 S* 609

FIG. 6

gtgcctac atg gtc acg tcc ttc cta gat aat gga cac ggg gaa tgt ttg	50
Met Val Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu	
1 5 10	
atg gac aag ccc cag aat cca atc aag ctc cct tct gat ctt ccc ggt	98
Met Asp Lys Pro Gln Asn Pro Ile Lys Leu Pro Ser Asp Leu Pro Gly	
15 20 25 30	
acc ttg tac gat gcc aac cgc cag tgt cag ttt aca ttc gga gag gaa	146
Thr Leu Tyr Asp Ala Asn Arg Gln Cys Gln Phe Thr Phe Gly Glu Glu	
35 40 45	
tcc aag cac tgc cct gat gca gcc agc aca tgt act acc ctg tgg tgc	194
Ser Lys His Cys Pro Asp Ala Ala Ser Thr Cys Thr Thr Leu Trp Cys	
50 55 60	
act ggc acc tcc ggt ggc tta ctg gtg tgc caa aca aaa cac ttc cct	242
Thr Gly Thr Ser Gly Gly Leu Leu Val Cys Gln Thr Lys His Phe Pro	
65 70 75	
tgg gca gat ggc acc agc tgt gga gaa ggg aag tgg tgt gtc agt ggc	290
Trp Ala Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Val Ser Gly	
80 85 90	
aag tgc gtg aac aag aca gac atg aag cat ttt gct act cct gtt cat	338
Lys Cys Val Asn Lys Thr Asp Met Lys His Phe Ala Thr Pro Val His	
95 100 105 110	
gga agc tgg gga cca tgg gga ccg tgg gga gac tgc tca aga acc tgt	386
Gly Ser Trp Gly Pro Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys	
115 120 125	
ggt ggt gga gtt caa tac aca atg aga gaa tgt gac aac cca gtc cca	434
Gly Gly Val Gln Tyr Thr Met Arg Glu Cys Asp Asn Pro Val Pro	
130 135 140	
aag aac gga ggg aag tac tgt gaa ggc aaa cga gtc cgc tac agg tcc	482
Lys Asn Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser	
145 150 155	
tgt aac atc gag gac tgt cca gac aat aac gga aaa acg ttc aga gag	530
Cys Asn Ile Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu	
160 165 170	
gag cag tgc gag gcg cac aat gag ttt tcc aaa gct tcc ttt ggg aat	578
Glu Gln Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Asn	
175 180 185 190	
gag ccc act gta gag tgg aca ccc aag tac gcc ggc gtc tcg cca aag	626
Glu Pro Thr Val Glu Trp Thr Pro Lys Tyr Ala Gly Val Ser Pro Lys	
195 200 205	

FIG. 7A

gac agg tgc aag ctc acc tgt gaa gcc aaa ggc att ggc tac ttt ttc		674	
Asp Arg Cys Lys Leu Thr Cys Glu Ala Lys Gly Ile Gly Tyr Phe Phe			
210	215	220	
gtc tta cag ccc aag gtt gta gat ggc act ccc tgt agt cca gac tct		722	
Val Leu Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser			
225	230	235	
acc tct gtc tgt gtg caa ggg cag tgt gtg aaa gct ggc tgt gat cgc		770	
Thr Ser Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg			
240	245	250	
atc ata gac tcc aaa aag aag ttt gat aag tgt ggc gtt tgt gga gga		818	
Ile Ile Asp Ser Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly			
255	260	265	270
aac ggt tcc aca tgc aag aag atg tca gga ata gtc act agt aca aga		866	
Asn Gly Ser Thr Cys Lys Lys Met Ser Gly Ile Val Thr Ser Thr Arg			
275	280	285	
cct ggg tat cat gac att gtc aca att cct gct gga gcc acc aac att		914	
Pro Gly Tyr His Asp Ile Val Thr Ile Pro Ala Gly Ala Thr Asn Ile			
290	295	300	
gaa gtg aaa cat cgg aat caa agg ggg tcc aga aac aat ggc agc ttt		962	
Glu Val Lys His Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe			
305	310	315	
ctg gct att aga gcc gct gat ggt acc tat att ctg aat gga aac ttc		1010	
Leu Ala Ile Arg Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asn Phe			
320	325	330	
act ctg tcc aca cta gag caa gac ctc acc tac aaa ggt act gtc tta		1058	
Thr Leu Ser Thr Leu Glu Gln Asp Leu Thr Tyr Lys Gly Thr Val Leu			
335	340	345	350
agg tac agt ggt tcc tcg gct gcg ctg gaa aga atc cgc agc ttt agt		1106	
Arg Tyr Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser			
355	360	365	
cca ctc aaa gaa ccc tta acc atc cag gtt ctt atg gta ggc cat gct		1154	
Pro Leu Lys Glu Pro Leu Thr Ile Gln Val Leu Met Val Gly His Ala			
370	375	380	
ctc cga ccc aaa att aaa ttc acc tac ttt atg aag aag aca gag		1202	
Leu Arg Pro Lys Ile Lys Phe Thr Tyr Phe Met Lys Lys Lys Thr Glu			
385	390	395	
tca ttc aac gcc att ccc aca ttt tct gag tgg gtg att gaa gag tgg		1250	
Ser Phe Asn Ala Ile Pro Thr Phe Ser Glu Trp Val Ile Glu Glu Trp			
400	405	410	

FIG. 7B

ggg gag tgc tcc aag aca tgc ggc tca ggt tgg cag aga aga gta gtg 1298
 Gly Glu Cys Ser Lys Thr Cys Gly Ser Gly Trp Gln Arg Arg Val Val
 415 420 425 430

 cag tgc aga gac att aac gga cac cct gct tcc gaa tgt gca aag gaa 1346
 Gln Cys Arg Asp Ile Asn Gly His Pro Ala Ser Glu Cys Ala Lys Glu
 435 440 445

 gtg aag cca gcc agt acc aga cct tgt gca gac ctt cct tgc cca cac 1394
 Val Lys Pro Ala Ser Thr Arg Pro Cys Ala Asp Leu Pro Cys Pro His
 450 455 460

 tgg cag gtg ggg gat tgg tca cca tgt tcc aaa act tgc ggg aag ggt 1442
 Trp Gln Val Gly Asp Trp Ser Pro Cys Ser Lys Thr Cys Gly Lys Gly
 465 470 475

 tac aag aag aga acc ttg aaa tgt gtg tcc cac gat ggg ggc gtg tta 1490
 Tyr Lys Lys Arg Thr Leu Lys Cys Val Ser His Asp Gly Gly Val Leu
 480 485 490

 tca aat gag agc tgt gat cct ttg aag aag cca aag cat tac att gac 1538
 Ser Asn Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Tyr Ile Asp
 495 500 505 510

 ttt tgc aca ctg aca cag tgc agt taagaggcgt tagaggacaa ggttagcgtgg 1592
 Phe Cys Thr Leu Thr Gln Cys Ser
 515

 ggagggggctg atacactgag tgcaagagta ctggagggat ccagttagtc aaaccagtaa 1652
 gcagttaggt gtggcaagga ggtgtgtta ggggatacat agcaaaggag gtagatcagg 1712
 acactaccct gccagttaca ttctgtataag gtatgttaatg aggacacagta gcatctgaaa 1772
 gaccatacag agcactaagg agccccaaag cactattagt atctctttc ttatatctat 1832
 cgcccaaata attttcagag tctggcagaa gcccgtgtc actgtactaa ctagatactt 1892
 cttatcacaa agattggaa aggccaaagca gaaagatggt aagactgggt ttcaaacaag 1952
 gcttggttgc aatcaactgga ggcaaggagg aggggacaaa caagatcatt attcgaagtc 2012
 gctggttgct gtggtttac ggaagggttga tgcatttc ctagataacag tgaaaaggtc 2072
 agcttgttca acgtgacaga aaggctcatc tccgtgaaag agctcctgat ttcttcttac 2132
 accatctcag ttcttaacta tagttcatgt tgaggttagaa acaattcatc tatttataaa 2192
 atgtacattt gaaaaaaaaa gtgaagttt tgaggtacac ataaaaactg aaggaaacaa 2252
 tgagcaacat gcctcctgct ttgcttcctc ctgaggtaaa cctgcctggg gattgaggtt 2312
 gtttaagatt atccatggct cacaagaggc agtaaaataa tacatgttgc gccagagtt 2372
 gaatggggta tagagatcag ggtcccatga gatggggAAC atgtgtatca ctcatttcac 2432
 atgggaggct gctgcagggt agcagggtcca ctccgtggcag ctggccaaac agtcgtatcc 2492
 tggtagatgt ctgttcagct cttctactga gagagaatat gactgtttcc atatgtat 2552
 gtatataatgta aaatatgtta ctatgtattt catgtactt ataagtattt gtgtgtctgt 2612
 tccttctaag aaggactata gtttataata aatgcctata ataacatatt tattttata 2672
 catttatttc taatgataaa acctttaagt tatatcgctt ttgtaaaagt gcatataaaa 2732
 atagagtatt tatacaatat atgttaacta gaaataataa aagaacactt ttgaatgtgt 2792
 atgccttattt tctggaggtgg gattaactt tgggcaagaa atctgtatgag acacaaacat 2852
 tggacttcaa gacagttta aatttgggt aaatgaactg tatttcctgt ttatagacgt 2912
 actaataaaa aagaagttga tgatgtctt agtggtaaga ttgttactaa tgggttggc 2972
 aaattgtgt aaagagccag atagtaagca tttatggcat tggtaggtat ctttcctgcc 3032
 acaaccatgt gacagttagt gctttgttagg actgagagca gccataaatg acatgtaaat 3092
 gataaaactgt ggctgtgtt taataaaaact ttatattacaa aaaaaaaaaaaa aaa 3145

gcggccgctc ccggccggcc caagggacag agccaggctc cgggagcccc caacactcgt 60
 cctgagagcc ccggctcctc agcccgctac gcccagggcc tcggcctccg ccccccactc 120
 ccgagctctt gccttagagt cgactggct cccgccccgcg tggcacagac agacggacag 180
 ccagccctgc gagggcgcgc ggaccgggcg gaggtgttgtt aggaggagac cgaggagggg 240
 ggctggctg gggctggggc cgcccccga agagagacat gcgattgtg accaagccga 300
 gcggacggac agcgccggcc ag atg cag gtg agc gag agg atg ctg gca ggg 352
 Met Gln Val Ser Glu Arg Met Leu Ala Gly
 1 5 10

ggt atg aga agc atg ccc agc ccc ctc ctg gcc tgc tgg cag ccc atc 400
 Gly Met Arg Ser Met Pro Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile
 15 20 25

ctc ctg ctg gta ctg ggc tca gtg ctg tca ggc tct gct aca ggc tgc 448
 Leu Leu Leu Val Leu Gly Ser Val Leu Ser Gly Ser Ala Thr Gly Cys
 30 35 40

ccg ccc cgc tgc gag tgc tca gcg cag gac cga gcc gtg ctc tgc cac 496
 Pro Pro Arg Cys Glu Cys Ser Ala Gln Asp Arg Ala Val Leu Cys His
 45 50 55

cgc aaa cgc ttt gtg gcg gtg ccc gag ggc atc ccc acc gag act cgc 544
 Arg Lys Arg Phe Val Ala Val Pro Glu Gly Ile Pro Thr Glu Thr Arg
 60 65 70

ctg ctg gac ctg ggc aaa aac cgc atc aag aca ctc aac cag gac gag 592
 Leu Leu Asp Leu Gly Lys Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu
 75 80 85 90

ttt gcc agc ttc cca cac ctg gag gag cta gaa ctc aat gaa aac atc 640
 Phe Ala Ser Phe Pro His Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile
 95 100 105

gtg agc gcc gtg gag cca ggc gcc ttc aac aac ctc ttc aac ctg agg 688
 Val Ser Ala Val Glu Pro Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg
 110 115 120

act ctg ggg ctg cgc agc aac cgc ctg aag ctt atc ccg ctg ggc gtc 736
 Thr Leu Gly Leu Arg Ser Asn Arg Leu Lys Leu Ile Pro Leu Gly Val
 125 130 135

ttc acc ggc ctc agc aac ttg acc aag ctg gac atc agt gag aac aag 784
 Phe Thr Gly Leu Ser Asn Leu Thr Lys Leu Asp Ile Ser Glu Asn Lys
 140 145 150

atc gtc atc ctg cta gac tac atg ttc caa gac cta tac aac ctc aag 832
 Ile Val Ile Leu Leu Asp Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys
 155 160 165 170

tcg ctg gag gtc ggc gac aac gac ctc gtc tac atc tcc cat cga gcc 880
 Ser Leu Glu Val Gly Asp Asn Asp Leu Val Tyr Ile Ser His Arg Ala
 175 180 185

FIG. 8A

ttc agc ggc ctc aac aac	ctg gaa cag ctg acg	ctg gag aaa tgc aat	928
Phe Ser Gly Leu Asn Ser	Leu Glu Gln Leu Thr	Leu Glu Lys Cys Asn	
190	195	200	
ctg acc tcc atc ccc acg gag	gag gcg ctc tcc cac	ctg cac ggc ctc atc	976
Leu Thr Ser Ile Pro Thr	Glu Ala Leu Ser His	Leu His Gly Leu Ile	
205	210	215	
gtc ctg cgg cta cga cat	ctc aac atc aat gcc atc	agg gac tac tcc	1024
Val Leu Arg Leu Arg His	Leu Asn Ile Asn Ala	Ile Arg Asp Tyr Ser	
220	225	230	
ttc aag agg ctg tac cga	ctt aag gtc tta gag atc	tcc cac tgg ccc	1072
Phe Lys Arg Leu Tyr Arg	Leu Lys Val Leu Glu	Ile Ser His Trp Pro	
235	240	245	250
tac ctg gac acc ata acc	ccc cgg acg cgt	ggg tcg ac	1110
Tyr Leu Asp Thr Ile Thr	Pro Arg Thr Arg	Gly Ser	
255	260		

FIG. 8B

ctcctggatg tgccgcagccg cagagcgtcg ctgcgtgtgcc taatacccat cgctgcgcac 60
 ttgacagcca gtccgccccgt ccggagccccg gctcgttggg gcagc atg gcg ggg tcg 117
 Met Ala Gly Ser
 1
 ccg ctg ctc tgc ggg ccg cgg gcc ggg ggc gtc ggc att ttg gtg ctg 165
 Pro Leu Leu Cys Gly Pro Arg Ala Gly Val Gly Ile Leu Val Leu
 5 10 15 20
 ctg ctc ttg ggc ctt ctg agg ctg ccc ccc acc ctg tca gcg agg ccc 213
 Leu Leu Leu Gly Leu Leu Arg Leu Pro Pro Thr Leu Ser Ala Arg Pro
 25 30 35
 gtg aag gag ccc cgc agt ctg agc gca gca tcc gcg ccc ttg gtt gag 261
 Val Lys Glu Pro Arg Ser Leu Ser Ala Ala Ser Ala Pro Leu Val Glu
 40 45 50
 acg agc act ccc ctc cgc ttg cgt cgg gcc gtc ccc cga gga gag gcg 309
 Thr Ser Thr Pro Leu Arg Leu Arg Arg Ala Val Pro Arg Gly Glu Ala
 55 60 65
 gcg ggt gcg gtg cag gag ctg gcg cgg gcg ctg gcg cac ctg ctg gag 357
 Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala His Leu Leu Glu
 70 75 80
 gcc gag aga cag gaa cgc gcg cgt gct gag gcg cag gag gct gag gat 405
 Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln Glu Ala Glu Asp
 85 90 95 100
 cag cag gcg cgt gtc ctg gcg cag ctg ctg cgc gcc tgg ggc tct ccg 453
 Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Ala Trp Gly Ser Pro
 105 110 115
 cgt gcc tcg gac ccg ccc ttg gcc ccc gac gat gac ccg gac gct cca 501
 Arg Ala Ser Asp Pro Pro Leu Ala Pro Asp Asp Pro Asp Ala Pro
 120 125 130
 gct gca cag ctc gcc cgt gct ctg ctc cga gct cgc cta gac ccc ggc 549
 Ala Ala Gln Leu Ala Arg Ala Leu Leu Arg Ala Arg Leu Asp Pro Gly
 135 140 145
 ccc cag tgt atg atg atg gcc cca ctg gcc cag acg tcg agg atg ccg 597
 Pro Gln Cys Met Met Ala Pro Leu Ala Gln Thr Ser Arg Met Pro
 150 155 160
 gcg acg aga ctc ctg acg tgg acc ctg acg tgc tgaggtaatt gctagggcgg 650
 Ala Thr Arg Leu Leu Thr Trp Thr Leu Ser Cys
 165 170 175
 atcctcacccg gaagttcgga gccagaggct gctcctgccc cgcgcgcct ccggcgatct 710
 gtggaccagg atttgggtcc cgaggtgccc cctgagaacg tactggggc tctgctacgc 770
 gtcaaacgccc tggagaaccc ctgcgcgcag ggcgcggcac gccqccctct qccctccctqa 830

FIG. 9A

gcgctgcgtgc atcctgcacg ccctggAACCC caggagcgcc ccagcaACCC tgactccctg 890
ccagcacgtc caaggctgct taccggcagca acctccccatc ccctgagccc tcaataaaatg 950
ccatctgttag caaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 1010
aaaaaaaaaaaaaaa aaaaaaaaaaaa 1027

FIG. 9B